IN THE SPECIFICATION:

[0042] FIG. 1. Structure-based sequence alignment of a selected number of bromodomains. The sequences were aligned based on the NMR-derived structure of the P/CAF bromodomain, and the predicated four a-helices are shown in green boxes. Bromodomains are grouped on the basis of the sequence and/or functional similarities as described by Jeanmougin et al., [Trends in Biochemical Sciences, 22:151-153 (1997)]. Residue numbers of the P/CAF bromodomain are indicated above its sequence. Three absolutely conserved residues, corresponding to Pro751, Pro767, and Asn803 in the P/CAF bromodomain, are shown in red. Highly conserved residues are colored in blue. The residues of the P/CAF bromodomain that interact with acetyl-histamine, as determined by intermolecular NOEs, are indicated by asterisks. The ZA loop, which is critical for acetyl-lysine binding, for each of the indicated bromodomains is also identified. The underlined residues were changed individually by site-directed mutagenesis to Ala. Genbank accession numbers for the proteins are as indicated in Table 8, in the Example below, along with the SEQ ID NOs. for the bromodomain sequences. Specifically, hsp/CAF (SEQ ID NO:7), hsGCN5 (SEQ ID NO:8), ttP55 (SEQ ID NO:9), scGCN5 (SEQ ID NO:10), hsP300 (SEQ ID NO:11), hsCBP (SEQ ID NO:12), mmCBP (SEQ ID NO:13), ceYNJ1 (SEQ ID NO:14), hsCCG1-1 (SEQ ID NO:15), msCCG1-1 (SEQ ID NO:16), hsCCG1-2 (SEQ ID NO:17), msCCG1-2 (SEQ ID NO:18), hsRing3-1 (SEQ ID NO:19), hsOREX-1 (SEQ ID NO:20), dmFSH-1 (SEQ ID NO:21), hsBR140 (SEQ ID NO:27), hsSMAP (SEQ ID NO:28), ggPB1-1 (SEQ ID NO:29), ggPB1-2 (SEQ ID NO:30), ggPB1-3 (SEQ ID NO:31), ggPB1-4 (SEQ ID NO:32), ggPB1-5 (SEQ ID NO:33), spBRO-1 (SEQ ID NO:34), spBRO-2 (SEQ ID NO:35), hsSNf2a (SEQ ID NO:36), hsBRGL (SEQ ID NO:37), ggBRM (SEQ ID NO:38), ggBRG1 (SEQ ID NO:39), hsTIF1b (SEQ ID NO:40), mmTIF1b (SEQ ID NO:41), and mmTIF1a (SEQ ID NO:42) are exemplified.